Ovary-Specific Genes and Proteins

Background of the Invention

1. Field of the Invention

The present invention relates generally to ovary-specific genes and the proteins they encode.

2. Description of Related Art

Reproductive development and function are complex processes involving both genetically-determined and physiological events. Identification of the critical protein products of genes involved in these processes is necessary to characterize how these processes are regulated. Although important molecular events occur during the early phases of mammalian oogenesis and folliculogenesis, to date, few "candidate" regulatory molecules have been identified and characterized thoroughly. Several studies have suggested that both endocrine factors, such luteinizing hormone (LH) and follicle stimulating hormone (FSH) from the pituitary, as well as paracrine factors secreted from the oocyte influence folliculogenesis. FSH and LH are known to bind to granulosa and thecal cells which in turn are required for oocyte growth and maturation and maintenance of oocyte meiotic competence. Likewise, oocytes may secrete factors which are necessary for normal granulosa cell and thecal cell function. Because oocyte growth is coordinated with the development and growth of the surrounding somatic cells (*i.e.*, granulosa cells initially and thecal cells later), understanding the molecular events at early stages will give important clues about the paracrine factors mediating the reciprocal interactions between oocytes and somatic cells, the development of competence for trophic hormone stimulation, and the process of follicular recruitment.

Disruption of the hypothalamic-pituitary-gonadal reproductive axis by administration of steroids containing synthetic estrogens and progestins has been one of the oldest methods of hormonal contraception. However, the latest report of the Institute of Medicine emphasizes the importance of developing strategies for new contraceptives. According to the report, some of the long-term contraceptive strategies for women include inhibition of ovulation, prevention of fertilization, or blocking of implantation of a fertilized egg into the uterine lining. Furthermore, infertility affects ~15% of couples,

and in ~40% of the cases, the female is believed to be the sole cause of the infertility. Thus, it is critical to identify novel ovary-specific gene products which could be potential targets for new contraceptive agents.

To identify key proteins in the hypothalamic-pituitary-gonadal axis, we have previously generated several important knockout mouse models, including four which have ovarian defects. Mice deficient in gonadal/pituitary peptide inhibin have secondary infertility due to the onset of ovarian or testicular tumors which appear as early as 4 weeks of age (Matzuk, et al., 1992). Mice deficient in activin receptor type II (ActRII) survive to adulthood but display reproductive defects. Male mice show reduced testes size and demonstrate delayed fertility (Matzuk, et al. 1995). In contrast, female mice have a block in folliculogenesis at the early antral follicle stage leading to infertility. Consistent with the known role of activins in FSH homeostasis, both pituitary and serum FSH levels are dramatically reduced in these ActRII knockout mice. Female mice deficient in FSH, due to a mutation in the FSHβ gene, are infertile (Kumar et al., 1997). However, these mice have an earlier block in folliculogenesis prior to antral follicle formation. Thus, FSH is not required for formation of a multi-layer pre-antral follicle, but it is required for progression to antral follicle formation. Finally, growth differentiation factor 9 (GDF-9)-deficient mice have been used to determine at which stage in follicular development GDF-9 is required (Dong et al., 1996). Expression of GDF-9 mRNA is limited to the oocyte and is seen at the early one-layer primary follicle stage and persists through ovulation. Absence of GDF-9 results in ovaries that fail to demonstrate any normal follicles beyond the primary follicle stage. Although oocytes surrounded by a single layer of granulosa cells are present and appear normal histologically, no normal two-layered follicles are present. Follicles beyond the one-layer stage are abnormal, contain atypical granulosa cells, and display asymmetric growth of these cells. Furthermore, as determined by light and electron microscopy, a thecal cell layer does not form in these GDF-9-deficient ovaries. Thus, in contrast to kit ligand and other growth factors which are synthesized by the somatic cells and influence oocyte growth, GDF-9 functions in the reciprocal manner as an oocyte-derived growth factor which is required for somatic cell function. The novel ovary-specific gene products presented herein are

expected to function in similar ways to regulate oogenesis and/or somatic cell function (e.g., folliculogenesis)

Summary of the Invention

The present invention provides three ovary-specific and oocyte-specific genes, O1-180, O1-184 and O1-236, the protein products they encode, fragments and derivatives thereof, and antibodies which are immunoreactive with these protein products. These genes and their protein products appear to relate to various cell proliferative or degenerative disorders, especially those involving ovarian tumors, such as germ cell tumors and granulosa cell tumors, or infertility, such as premature ovarian failure.

Thus, in one embodiment, the invention provides methods for detecting cell proliferative or degenerative disorders of ovarian origin and which are associated with O1-180, O1-184 or O1-236. In another embodiment, the invention provides method of treating cell proliferative or degenerative disorders associated with abnormal levels of expression of O1-180, O1-184 or O1-236, by suppressing or enhancing their respective activities.

The present invention provides key *in vitro* and *in vivo* reagents for studying ovarian development and function. The possible applications of these reagents are far-reaching, and are expected to range from use as tools in the study of development to therapeutic reagents against cancer. The major application of these novel ovarian gene products is to us them as reagents to evaluate potential contraceptives to block ovulation in women in a reversible manner. It will also be expected that these novel ovarian gene products will be useful to screen for genetic mutations in components of these signaling pathways that are associated with some forms of human infertility or gynecological cancers. In addition, depending on the phenotypes of humans with mutations in these genes or signaling pathways, we may consider using these novel ovarian gene products as reagent tools to generate a number of mutant mice for the further study of oogenesis and/or folliculogenesis. Such knockout mouse models will provide key insights into the roles of these gene products in human female reproduction and permit the use of these gene products as practical reagents for evaluation of new contraceptives.

Brief Description of the Drawings

FIG. 1 shows the 1276 base pair cDNA sequence of gene O1-180

FIG. 2 shows the 361 amino acid sequence that is coded for by gene O1-180.

FIG. 3 shows the 1817 base pair cDNA sequence of gene O1-184.

FIG. 4 shows the 426 amino acid sequence that is coded for by gene O1-184.

FIG. 5 shows the 1019 base pair cDNA sequence of gene O1-236.

FIG. 6 shows the 207 amino acid sequence that is coded for by gene O1-236.

FIG. 7. Multi-tissue Northern blot analysis of ovary-specific genes. Northern blot analysis was performed on total RNA using O1-180, O1-184, and O1-236 probes. These gene products demonstrate an ovary-specific pattern (OV, ovary; WT, wild-type; -/-, GDF-9-deficient) as shown. The migration positions of 18S and 28S ribosomal RNA are indicated. All lanes had approximately equal loading as demonstrated using an 18S rRNA cDNA probe. Br, brain; Lu, lung; He, heart; St, stomach; Sp, spleen; Li, liver; SI, small intestine; Ki, kidney; Te, testes, Ut, uterus.

FIG. 8. In situ hybridization analysis of ovary-specific genes in mouse ovaries. In situ hybridization was performed using anti-sense probes to O1-180 (A, B), O1-184 (C,D) and O1-236 (E,F). A, C, and E are brightfield analysis of the ovaries. B, D, and F are darkfield analysis of the same ovary sections. All genes demonstrate specific expression in the oocyte beginning at the one layer primary follicle stage (small arrows) and continuing through the antral follicle stage (large arows). The "sense" probe does not detect a signal for any of these three ovary-specific genes (data not shown).

FIG. 9. In situ hybridization analysis of O1-236 in mouse ovaries. In situ hybridization was performed using probe O1-236 (partial *Npm2* fragment). Brightfield analysis (A) and darkfield analysis (B) of the O1-236 mRNA in the same adult ovary sections. The probe demonstrates specific expression in all growing oocytes. Oocyte-specific expression is first seen in the early one layer primary follicle (type 3a), with higher expression in the one layer type 3b follicle and all subsequent stages including antral (an) follicles. The "sense" probe does not detect a signal for this oocyte-specific gene (data not shown).

FIG. 10. Npm2 cDNA representation. Schematic representation of the mouse *Npm2* cDNA sequence (984 bp) and two of the clones isolated from the mouse ovary

CDNA libraries. The original 01-236 probe (749 bp) is shown at the top and encompasses the entire *Npm2* open reading frame. The open reading frame (solid box) is 621 bp and the 5' UTR and 3' UTR sequences (thin lines) are 155 bp and 205 bp, respectively. The polyA sequences are not depicted. Clone 236-1 was isolated from the wild-type ovary cDNA library and clone 236-3 was isolated from the GDF-9-deficient ovary cDNA library. Clone 236-3 (984 bp excluding polyA sequence) is 4 bp longer at the 5' end and 1 bp longer at the 3' end than clone 236-1 (979 bp excluding polyA sequences). Codon 36 of the open reading frame of both cDNAs is GGC (Glycine; Figure 11) whereas the same codon of the 129SvEv gene is TGC (Cysteine; Figure 13).

FIG. 11. Amino acid sequence conservation between mouse Npm2 and *Xenopus laevis* nucleoplasmin (Xnpm2). Using the NCB1 blast search tools, comparison of mouse Npm2 and Xnpm2 (accession # P05221) amino acid sequences reveals high identity (line connecting amino acids) and similarity (dots connecting amino acids). Spaces between the amino acids indicate gaps to aid in the alignment. Also identified are the conserved bipartite nuclear localization signal (bolded and underlined), the highly acidic "histone binding" region (boxed), and several conserved casein kinase II (CK2) and protein kinase C (PKC) phosphorylation sites (underlined and marked with "CK" or "PKC" with the serine or threonine in bold). Other predicted phosphorylation sites in either Npm2 or Xnpm2, which are not conserved, are not shown.

FIG. 12. Structure of the mouse *Npm2* gene. Two overlapping recombinant λ clones (236-13 and 236-14), isolated from a mouse 129SvEv library, are shown at the top, and a schematic enlargement of the *Npm2* gene is also depicted. Open boxes represent untranslated regions and solid black boxes represent protein coding regions. The 236-13 insert is ~19.0 kb and 236-14 insert is ~21.0 kb. The entire contig is ~37 kb. All 9 exons of the *Npm2* gene are encompassed on a single 6.9 kb XbaI (X) fragment as shown. The size of exons and introns are shown at the bottom. Abbreviations: B, BamH1; (B), predicted but unmapped BamH1; (N), NotI from phage cloning site.

FIG. 13. Mouse *Npm2* gene and amino acid sequences. Uppercase letters represent sequence identity with the *Npm2* cDNA sequences; non-transcribed 5' and 3' sequences and intron sequences are shown in lowercase. The predicted transcription initiation codon, the termination codon, and the polyadenylation signal sequence are all

underlined. Numbers along the left side represent the amino acids. The underlined and bloded "T" in codon 36, the bolded "C" for amino acid 26, and the underlined and bolded "C" in the 3' UTR sequence indicate differences between the cDNA and gene sequences. Arrows indicate where the O1-236 fragment initiates and ends in the cDNA sequence.

FIG. 14. Chromosomal localization of the mouse Npm2 gene. (Top) Map figure from the T31 radiation hybrid database at The Jackson Laboratory showing Chromosome 14 data. The map is depicted with the centromere toward the top. Distances between adjacent loci in centiRay3000 are shown to the left of the chromosome bar. The positions of some of the chromosome 14 MIT markers are shown on the right. *Npm2* is positioned between D14Mit203 and D14Mit32. Missing typings were inferred from surrounding data where assignment was unambiguous. Raw data from The Jackson Laboratory were obtained from the Wold Wide Web address http://www.jax.org/resources/documents /cmdata/rhmap/rh.html. (Bottom) Haplotype figure from the T31 radiation hybrid database at The Jackson Laboratory showing part of Chromosome 14 with loci linked to *Npm2*. Loci are listed in the best fit order with the most proximal at the top. The black boxes represent hybrid cell lines scoring positive for the mouse fragment and the white boxes represent cell lines scoring as negative. The grey box indicates an untyped or ambiguous line. The number of lines with each haplotype is given at the bottom of each column of boxes. Missing typings were inferred from surrounding data where assignment was unambiguous.

Detailed Description of the Invention

The present invention provides three novel proteins, O1-180, O1-184, O1-236, the polynucleotide sequences that encode them, and fragments and derivatives thereof. Expression of O1-180, O1-184, O1-236 is highly tissue-specific, being expressed in cells primarily in ovarian tissue. In one embodiment, the invention provides a method for detection of a cell proliferative or degenerative disorder of the ovary, which is associated with expression of O1-180, O1-184 or O1-236. In another embodiment, the invention provides a method for treating a cell proliferative or degenerative disorder associated with abnormal expression of O1-180, O1-184, O1-236 by using an agent which suppresses or enhances their respective activities.

Based on the known activities of many other ovary specific proteins, it can be expected that O1-180, O1-184 and O1-236, as well as fragments and derivatives thereof, will also possess biological activities that will make them useful as diagnostic and therapeutic reagents.

For example, GDF-9 is an oocyte-expressed gene product which has a similar pattern of expression as O1-180, O1-184, and O1-236. We have shown that mice lacking GDF-9 are infertile at a very early stage of follicular development, at the one-layer primary follicle stage (Dong, et al.). These studies demonstrate that agents which block GDF-9 function would be useful as contraceptive agents in human females. Since O1-180, O1-184, and O1-236 have an expression pattern in the oocyte (Figure 8) which is nearly identical to GDF-9, this suggests that mice and humans or any other mammal lacking any of all of these gene products would also be infertile. Thus, blocking the function of any or all of these gene products would result in a contraceptive action.

Another regulatory protein that has been found to have ovary-specific expression is inhibin, a specific and potent polypeptide inhibitor of the pituitary secretion of FSH. Inhibin has been isolated from ovarian follicular fluid. Because of its suppression of FSH, inhibin has been advanced as a potential contraceptive in both males and females. O1-180, O1-184 and O1-236 may possess similar biological activity since they are also ovarian specific peptides. Inhibin has also been shown to be useful as a marker for certain ovarian tumors (Lappohn, et *al.*, *N. Engl. J. Med.*, 321:790, 1989). O1-180, O1-184, O1-236 may also be useful as markers for identifying primary and metastatic neoplasms of ovarian origin. Likewise, mice which lack inhibin develop granulosa cell tumors (Matzuk et al., 1992). Similarly, O1-180, O1-184 and O1-236 may be useful as indicators of developmental anomalies in prenatal screening procedures.

Mullerian inhibiting substance (MIS) peptide, which is produced by the testis and is responsible for the regression of the Mullerian ducts in the male embryo, has been shown to inhibit the growth of human ovarian cancer in nude mice (Donahoe, et al., *Ann. Surg.*, 194:472, 1981). O1-180, O1-184 and O1-236 may function similarly and may, therefore, be targets for anti-cancer agents, such as for the treatment of ovarian cancer.

O1-180, O1-184 and O1-236, and agonists and antagonists thereof can be used to identify agents which inhibit fertility (*e.g.*, act as a contraceptive) in a mammal (*e.g.*, human). Additionally, O1-180, O1-184 and O1-236 and agonists and antagonists thereof can be used to identify agents which enhance fertility (*e.g.*, increase the success of *in vivo* or *in vitro* fertilization) in a mammal. Likewise, assays of these or related oocyte-expressed gene products can be used in diagnostic assays for detecting forms of infertility (*e.g.*, in an assay to analyze activity of these gene products) or other diseases (*e.g.*, germ cell tumors, polycystic ovary syndrome).

O1-180, O1-184 and O1-236 or agents which act on these pathways may also function as growth stimulatory factors and, therefore, be useful for the survival of various cell populations *in vitro*. In particular, if O1-180, O1-184 and/or O1-236 play a role in oocyte maturation, they may be useful targets for *in vitro* fertilization procedures, e.g., in enhancing the success rate.

The term "substantially pure" as used herein refers to O1-180, O1-184 and O1-236 which are substantially free of other proteins, lipids, carbohydrates or other materials with which they are naturally associated. One skilled in the art can purify O1-180, O1-184 and O1-236 using standard techniques for protein purification. The substantially pure polypeptide will yield a single major band on a non-reducing polyacrylamide gel. The purity of the O1-180, O1-184 and O1-236 polypeptides can also be determined by amino-terminal amino acid sequence analysis. O1-180, O1-184 and O1-236 polypeptides includes functional fragments of the polypeptides, as long as their activities remain. Smaller peptides containing the biological activities of O1-180, O1-184 and O1-236 are included in the invention.

The invention provides polynucleotides encoding the O1-180, O1-184 and O1-236 proteins and fragments and derivatives thereof. These polynucleotides include DNA, cDNA and RNA sequences which encode O1-180, O1-184 or O1-236. It is understood that all polynucleotides encoding all or a portion of O1-180, O1-184

and/or O1-236 are also included herein, as long as they encode a polypeptide with the activity of O1-180, O1-184 or O1-236. Such polynucleotides include naturally occurring, synthetic, and intentionally manipulated polynucleotides. For example, polynucleotides of O1-180, O1-184 or O1-236 may be subjected to site-directed mutagenesis. The polynucleotide sequences for O1-180, O1-184 and O1-236 also includes antisense sequences. The polynucleotides of the invention include sequences that are degenerate as a result of the genetic code. There are 20 natural amino acids, most of which are specified by more than one codon. Therefore, all degenerate nucleotide sequences are included in the invention as long as the amino acid sequences of O1-180, O1-184 and O1-236 polypeptides encoded by the nucleotide sequences are functionally unchanged.

Minor modifications of the recombinant O1-180, O1-184 and O1-236 primary amino acid sequences may result in proteins which have substantially equivalent activity as compared to the respective O1-180, O1-184 and O1-236 polypeptides described herein. Such modifications may be deliberate, as by site-directed mutagenesis, or may be spontaneous. All of the polypeptides produced by these modifications are included herein as long as the biological activity of O1-180, O1-184 or O1-236 still exists. Further, deletion of one or more amino adds can also result in a modification of the structure of the resultant molecule without significantly altering its biological activity. This can lead to the development of a smaller active molecule which would have broader utility. For example, one could remove amino or carboxy terminal amino acids which may not be required for biological activity of O1-180, O1-184 or O1-236.

The nucleotide sequences encoding the O1-180, O1-184 and O1-236 polypeptides of the invention include the disclosed sequences and conservative variations thereof. The term"conservative variation" as used herein denotes the replacement of an amino acid residue by another, biologically similar residue. Examples of conservative variations include the substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as the substitution of arginine for lysine, glutamic acid for aspartic acid, or glutamine for

asparagine, and the like. The term "conservative variation" also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid provided that antibodies raised to the substituted polypeptide also immunoreact with the unsubstituted polypeptide.

For the purpose of this invention, the term "derivative" shall mean any molecules which are within the skill of the ordinary practitioner to make and use, which are made by derivatizing the subject compound, and which do not destroy the activity of the derivatized compound. Compounds which meet the foregoing criteria which diminish, but do not destroy, the activity of the derivatized compound are considered to be within the scope of the term "derivative." Thus, according to the invention, a derivative of a compound comprising amino acids in a sequence corresponding to the sequence of O1-180, O1-184 or O1-236, need not comprise a sequence of amino acids that corresponds exactly to the sequence of O1-180, O1-184 or O1-236, so long as it retains a measurable amount of the activity of the O1-180, O1-184 or O1-236 .

Fragments of proteins are seen to include any peptide that contains 6 contiguous amino acids or more that are identical to 6 contiguous amino acids of either of the sequences shown in Figures 2, 4, 6, 11 and 14. Fragments that contain 7, 8, 9, 10, 11, 12, 13, 14 and 15 or more contiguous amino acids or more that are identical to a corresponding number of amino acids of any of the sequences shown in Figures 2, 4, 6, 11 and 14 are also contemplated. Fragments may be used to generate antibodies. Particularly useful fragments will be those that make up domains of O1-180, O1-184 or O1-236. Domains are defined as portions of the proteins having a discrete tertiary structure and that is maintained in the absence of the remainder of the protein. Such structures can be found by techniques known to those skilled in the art. The protein is partially digested with a protease such as subtilisin, trypsin, chymotrypsin or the like and then subjected to polyacrylamide gel electrophoresis to separate the protein fragments. The fragments can then be transferred to a PVDF membrane and subjected to micro sequencing to determine the amino acid sequence of the N-terminal of the fragments.

DNA sequences of the invention can be obtained by several methods. For example, the DNA can be isolated using hybridization or amplification techniques which are well known in the art. These include, but are not limited to: 1) hybridization of genomic or cDNA libraries with probes to detect homologous nucleotide sequences, 2) antibody screening of expression libraries to detect cloned DNA fragments with shared structural features, or 3) use of oligonucleotides related to these sequences and the technique of the polymerase chain reaction.

Preferably the O1-180, O1-184 and O1-236 polynucleotides of the invention are derived from a mammalian organism, and most preferably from a mouse, rat, pig, cow or human. Screening procedures which rely on nucleic acid hybridization make it possible to isolate any gene sequence from any organism, provided the appropriate probe is available. Oligonucleotide probes, which correspond to a part of the sequence encoding the protein in question, can be synthesized chemically. This requires that short, oligopeptide stretches of amino acid sequence must be known. The DNA sequence encoding the protein can be deduced from the genetic code, however, the degeneracy of the code must be taken into account. It is possible to perform a mixed addition reaction when the sequence is degenerate. This includes a heterogeneous mixture of denatured double-stranded DNA. For such screening, hybridization is preferably performed on either single-stranded DNA or denatured double-stranded DNA. Hybridization is particularly useful in the detection of cDNA clones derived from sources where an extremely low amount of mRNA sequences relating to the polypeptide of interest are present. In other words, by using stringent hybridization conditions directed to avoid non-specific binding, it is possible, for example, to allow the autoradiographic visualization of a specific cDNA done by the hybridization of the target DNA to that single probe in the mixture which is its complete complement (Wallace, et al., *Nucl. Acid Res.*, 9:879, 1981).

The development of specific DNA sequences encoding O1-180, O1-184 and O1-236 can also be obtained by: 1) isolation of double-stranded DNA sequences from the genomic DNA; 2) chemical manufacture of a DNA sequence to provide the necessary

codons for the polypeptides of interest; and 3) in vitro synthesis of a double stranded DNA sequence by reverse transcription of mRNA isolated from a eukaryotic donor cell. In the latter case, a double-stranded DNA complement of mRNA is eventually formed which is generally referred to as cDNA.

Of the three above-noted methods for developing specific DNA sequences for use in recombinant procedures, the isolation of genomic DNA isolates is the least common. This is especially true when it is desirable to obtain the microbial expression of mammalian polypeptides due to the presence of introns.

The synthesis of DNA sequences is frequently the method of choice when the entire sequence of amino acid residues of the desired polypeptide product is known. When the entire sequence of amino acid residues of the desired polypeptides is not known, the direct synthesis of DNA sequences is not possible and the method of choice is the synthesis of cDNA sequences. Among the standard procedures for isolating cDNA sequences of interest is the formation of plasmid- or phage-carrying cDNA libraries which are derived from reverse transcription of mRNA which is abundant in donor cells that have a high level of genetic expression. When used in combination with polymerase chain reaction technology, even rare expression products can be cloned. In those cases where significant portions of the amino acid sequence of the polypeptide are known, the production of labeled single or double-stranded DNA or RNA probe sequences duplicating a sequence putatively present in the target cDNA may be employed in DNA/DNA hybridization procedures which are carried out on cloned copies of the cDNA which have been denatured into a single-stranded form (Jay, et al., *Nucl. Acid Res.*, 11:2325, 1983).

A cDNA expression library, such as lambda gt11, can be screened indirectly for O1-180, O1-184 and/or O1-236 peptides having at least one epitope, using antibodies specific for O1-180, O1-184 and/or O1-236 . Such antibodies can be either polyclonally or monoclonally derived and used to detect expression product indicative of the presence of O1-180, O1-184 and/or O1-236 cDNA.

DNA sequences encoding O1-180, O1-184 or O1-236 can be expressed *in vitro* by DNA transfer into a suitable host cell. "Host cells" are cells in which a vector can be propagated and its DNA expressed. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used. Methods of stable transfer, meaning that the foreign DNA is continuously maintained in the host, are known in the art.

In the present invention, the O1-180, O1-184 and/or O1-236 polynucleotide sequences may be inserted into a recombinant expression vector. The term "recombinant expression vectors" refers to a plasmid, virus or other vehicle known in the art that has been manipulated by insertion or incorporation of the O1-180, O1-184 or O1-236 genetic sequences. Such expression vectors contain a promoter sequence which facilitates the efficient transcription of the inserted genetic sequence of the host. The expression vector typically contains an origin of replication, a promoter, as well as specific genes which allow phenotypic selection of the transformed cells. Vectors suitable for use in the present invention include, but are not limited to the T7-based expression vector for expression in bacteria (Rosenberg, et al.,*Gene* ,56:125, 1987), the pMSXND expression vector for expression in mammalian cells (Lee and Nathans, J. *Biol. Chem.*, 263:3521, 1988) and baculovirus-derived vectors for expression in insect cells. The DNA segment can be present in the vector operably linked to regulatory elements, for example, a promoter (e.g., T7, metallothionein 1, or polyhedrin promoters). Polynucleotide sequences encoding O1-180, O1-184 or O1-236 can be expressed in either prokaryotes or eukaryotes. Hosts can include microbial, yeast, insect and mammalian organisms. Methods of expressing DNA sequences having eukaryotic or viral sequences in prokaryotes are well known in the art. Biologically functional viral and plasmid DNA vectors capable of expression and replication in a host are known in the art. Such vectors are used to incorporate DNA sequences of the invention.

Transformation of a host cell with recombinant DNA may be carried out by conventional techniques as are well known to those skilled in the art. Where the host is prokaryotic, such as E *coli,* competent cells which are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by the $CaCl_2$ method using procedures well known in the art. Alternatively, $MgCl_2$ or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired.

When the host is a eukaryote, such methods of transfection of DNA as calcium phosphate co-precipitates, conventional mechanical procedures such as microinjection, electroporation, insertion of a plasmid encased in liposomes, or virus vectors may be used. Eukaryotic cells can also be co-transformed with DNA sequences encoding the O1-180, O1-184 or O1-236 cDNA sequences of the invention, and a second foreign DNA molecule encoding a selectable phenotype, such as the neomycin resistance gene. Another method is to use a eukaryotic viral vector, such as simian virus 40 (SV40) or bovine papilloma virus, to transiently infect or transform eukaryotic cells and express the protein. (see for example, *Eukaryotic Viral Vectors,* Cold Spring Harbor Laboratory, Gluzman ed., 1982).

Isolation and purification of microbial expressed polypeptide, or fragments thereof, provided by the invention, may be carried out by conventional means induding preparative chromatography and immunological separations involving monoclonal or polyclonal antibodies.

The invention includes antibodies immunoreactive with O1-180, O1-184 or O1-236 polypeptides or functional fragments thereof. Antibody which consists essentially of pooled monoclonal antibodies with different epitopic specificities, as well as distinct monoclonal antibody preparatory are provided. Monoclonal antibodies are made from antigen containing fragments of the protein by methods well known to those skilled in the art (Kohler, et al., *Nature*, 256:495, 1975). The term antibody as used in this invention is meant to include intact molecules as well as fragments thereof, such as Fab

and F(ab')2, which are capable of binding an epitopic determinant on O1-180, O1-184 or O1-236 .

The term "cell-proliferative disorder" denotes malignant as well as non-malignant cell populations which often appear to differ from the surrounding tissue both morphologically and genotypically. The O1-180, O1-184 and O1-236 polynucleotides that are antisense molecules are useful in treating malignancies of the various organ systems, particularly, for example, the ovaries. Essentially, any disorder which is etiologically linked to altered expression of O1-180, O1-184 or O1-236 could be considered susceptible to treatment with a O1-180, O1-184 or O1-236 suppressing reagent, respectively.

The invention provides a method for detecting a cell proliferative disorder of the ovary which comprises contacting an anti-O1-180, O1-184 or O1-236 antibody with a cell suspected of having an O1-180, O1-184 or O1-236 associated disorder and detecting binding to the antibody. The antibody reactive with O1-180, O1-184 or O1-236 is labeled with a compound which allows detection of binding to O1-180, O1-184 or O1-236, respectively. For purposes of the invention, an antibody specific for an O1-180, O1-184 or O1-236 polypeptide may be used to detect the level of O1-180, O1-184 or O1-236, respectively, in biological fluids and tissues. Any specimen containing a detectable amount of antigen can be used. A preferred sample of this invention is tissue of ovarian origin, specifically tissue containing oocytes or ovarian follicular fluid. The level of O1-180, O1-184 or O1-236 in the suspect cell can be compared with the level in a normal cell to determine whether the subject has an O1-180, O1-184 or O1-236-associated cell proliferative disorder. Preferably the subject is human. The antibodies of the invention can be used in any subject in which it is desirable to administer in vitro or in vivo immunodiagnosis or immunotherapy. The antibodies of the invention are suited for use, for example, in immuno assays in which they can be utilized in liquid phase or bound to a solid phase carrier. In addition, the antibodies in these immunoassays can be detectably labeled in various ways. Examples of types of immunoassays which can utilize antibodies of the invention are competitive and non-

competitive immunoassays in either a direct or indirect format. Examples of such immunoassays are the radioimmunoassay (RIA) and the sandwich (ELISA) assay. Detection of the antigens using the antibodies of the invention can be done utilizing immunoassays which are run in either the forward, reverse, or simultaneous modes, including immunohistochemical assays on physiological samples. Those of skill in the art will know, or can readily discern, other immunoassay formats without undue experimentation.

The term "cell-degenerative disorder" denotes the loss of any type of cell in the ovary, either directly or indirectly. For example, in the absence of GDF-9, there is a block in the growth of the granulosa cells leading to eventual degeneration (*i.e.*, death) of the oocytes (Dong et al., 1996). This death of the oocyte appears to lead to differentiation of the granulosa cells. In addition, in the absence of GDF-9, no normal thecal cell layer is formed around the follicles. Thus, in the absence of one oocyte-specific protein, GDF-9, there are defects in three different cell lineages, oocytes, granulosa cells, and thecal cells. In a similar way, death or differentiation of these various cell lineages could be affected by absence or misexpression of O1-180, O1-184, or O1-236. Furthermore, absence or misexpression of O1-180, O1-184, or O1-236 could result in defects in the oocyte/egg leading to the inability of the egg to be fertilized by spermatozoa.

The antibodies of the invention can be bound to many different carriers and used to detect the presence of an antigen comprising the polypeptide of the invention. Samples of well-known carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magnetite. The nature of the carrier can be either soluble or insoluble for purposes of the invention. Those skilled in the art will know of other suitable carriers for binding antibodies, or will be able to ascertain such, using routine experimentation.

There are many different labels and methods of labeling known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present

invention include enzymes, radioisotopes, fluorescent compounds, colloidal metals, chemiluminescent compounds, phosphorescent compounds, and bioluminescent compounds. Those of ordinary skill in the art will know of other suitable labels for binding to the antibody, or will be able to ascertain such, using routine experimentation.

Another technique which may also result in greater sensitivity consists of coupling the antibodies to low molecular weight haptens. These haptens can then be specifically detected by means of a second reaction. For example, it is common to use such haptens as biotin, which reacts with avidin, or dinitrophenyl, puridoxal, and fluorescein, which can react with specific anti-hapten antibodies.

In using the monoclonal antibodies of the invention for the in vivo detection of antigen, the detectably labeled antibody is given a dose which is diagnostically effective. The term "diagnostically effective" means that the amount of detectably labeled monoclonal antibody is administered in sufficient quantity to enable detection of the site having the antigen composing a polypeptide of the invention for which the monoclonal antibodies are specific. The concentration of detectably labeled monoclonal antibody which is administered should be sufficient such that the binding to those cells having the polypeptide is detectable compared to the background. Further, it is desirable that the detectably labeled monoclonal antibody be rapidly cleared from the circulatory system in order to give the best target-to-background signal ratio. As a rule, the dosage of detectably labeled monoclonal antibody for in vivo diagnosis will vary depending on such factors as age, sex, and extent of disease of the individual. Such dosages may vary, for example, depending on whether multiple injections are given, antigenic burden, and other factors known to those of skill in the art.

For *in vivo* diagnostic imaging, the type of detection instrument available is a major factor in selecting a given radioisotope. The radioisotope chosen must have a type of decay which is detectable for a given type of instrument. Still another important factor in selecting a radioisotope for in vivo diagnosis is that deleterious radiation with

respect to the host is minimized. Ideally, a radioisotope used for in *vivo* imaging will lack a particle emission, but produce a large number of photons in the 140-250 keV range, which may readily be detected by conventional gamma cameras.

For *in vivo* diagnosis, radioisotopes may be bound to immunoglobulin either directly or indirectly by using an intermediate functional group. Intermediate functional groups which often are used to bind radioisotopes which exist as metallic ions to immunoglobulins are the bifunctional chelating agents such as diethylenetriaminepentacetic acid (DTPA) and ethylenediaminetetraacetic acid (EDTA) and similar molecules. Typical examples of metallic ions which can be bound to the monoclonal antibodies of the invention are ^{111}In, ^{97}Ru, ^{67}Ga, ^{68}Ga, ^{72}As, ^{89}Zr and ^{201}Ti.

The monoclonal antibodies of the invention can also be labeled with a paramagnetic isotope for purposes of *in vivo* diagnosis, as in magnetic resonance imaging (MRI) or electron spin resonance (ESR). In general, any conventional method for visualizing diagnostic imaging can be utilized. Usually gamma and positron emitting radioisotopes are used for camera imaging and paramagnetic isotopes for MRI. Elements which are particularly useful in such techniques include ^{157}Gd, ^{55}Mn, ^{162}Dy, ^{55}Cr and ^{56}Fe.

The monoclonal antibodies of the invention can be used *in vitro* and *in* vivo to monitor the course of amelioration of an O1-180, O1-184 or O1-236-associated disease in a subject. Thus, for example, by measuring the increase or decrease in the number of cells expressing antigen comprising a polypeptide of the invention or changes in the concentration of such antigen present in various body fluids, it would be possible to determine whether a particular therapeutic regimen aimed at ameliorating the O1-180, O1-184 or O1-236-associated disease is effective. The term "ameliorate" denotes a lessening of the detrimental effect of the O1-180, O1-184 or O1-236-associated disease in the subject receiving therapy.

The present invention identifies nucleotide sequences that can be expressed in an altered manner as compared to expression in a normal cell, therefore, it is possible to

design appropriate therapeutic or diagnostic techniques directed to this sequence. Thus, where a cell-proliferative disorder is associated with the expression of O1-180, O1-184 or O1-236, nucleic acid sequences that interfere with the expression of O1-180, O1-184 or O1-236, respectively, at the translational level can be used. This approach utilizes, for example, antisense nucleic acids or ribozymes to block translation of a specific O1-180, O1-184 or O1-236 mRNA, either by masking that mRNA with an antisense nucleic acid or by cleaving it with a ribozyme.

Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule (Weintraub, *Scientific American*, 262:40, 1990). In the cell, the antisense nucleic acids hybridize to the corresponding mRNA, forming a double-stranded molecule. The antisense nucleic acids interfere with the translation of the mRNA, since the cell will not translate a mRNA that is double-stranded. Antisense oligomers of about 15 nucleotides are preferred, since they are easily synthesized and are less likely to cause problems than larger molecules when introduced into the target O1-180, O1-184 or O1-236-producing cell. The use of antisense methods to inhibit the *in vitro* translation of genes is well known in the art (Marcus-Sakura, *Anal.Biochem.*, 172:289, 1988).

Ribozymes are RNA molecules possessing the ability to specifically cleave other single-stranded RNA in a manner analogous to DNA restriction endonucleases. Through the modification of nucleotide sequences which encode these RNAs, it is possible to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and cleave it (Cech, *J.Amer.Med. Assn.*, 260:3030, 1988). A major advantage of this approach is that, because they are sequence-specific, only mRNAs with particular sequences are inactivated.

There are two basic types of ribozymes namely, tetrahymena-type (Hasselhoff, *Nature*, 334:585, 1988) and "hammerhead"-type. Tetrahymena-type ribozymes recognize sequences which are four bases in length, while "hammerhead"-type ribozymes recognize base sequences 11-18 bases in length. The longer the recognition sequence,

the greater the likelihood that the sequence will occur exclusively in the target mRNA species. Consequently, hammerhead-type ribozymes are preferable to tetrahymena-type ribozymes for inactivating a specific mRNA species and 18-based recognition sequences are preferable to shorter recognition sequences.

The present invention also provides gene therapy for the treatment of cell proliferative or degenerative disorders which are mediated by O1-180, O1-184 or O1-236 proteins. Such therapy would achieve its therapeutic effect by introduction of the respective O1-180, O1-184 or O1-236 cDNAs or O1-180, O1-184, or O1-236 antisense polynucleotide into cells having the proliferative or degenerative disorder. Delivery of O1-180, O1-184, or O1-236 cDNAs or antisense O1-180, O1-184 or O1-236 polynucleotides can be achieved using a recombinant expression vector such as a chimeric virus or a colloidal dispersion system.

Especially preferred for therapeutic delivery of cDNAs or antisense sequences is the use of targeted liposomes.

Various viral vectors which can be utilized for gene therapy as taught herein include adenovirus, herpes virus, vaccinia, or, preferably, an RNA virus such as a retrovirus. Preferably, the retroviral vector is a derivative of a murine or avian retrovirus. Examples of retroviral vectors in which a single foreign gene can be inserted include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV). A number of additional retroviral vectors can incorporate multiple genes. All of these vectors can transfer or incorporate a gene for a selectable marker so that transduced cells can be identified and generated. By inserting an O1-180, O1-184 or O1-236 sequence of interest into the viral vector, along with another gene which encodes the ligand for a receptor on a specific target cell, for example, the vector is now target specific. Retroviral vectors can be made target specific by inserting, for example, a polynucleotide encoding a sugar, a glycolipid, or a protein. Preferred targeting is accomplished by using an antibody to target the retroviral vector.

Those of skill in the art will know of, or can readily ascertain without undue experimentation, specific polynucleotide sequences which can be inserted into the retroviral genome to allow target specific delivery of the retroviral vector containing a O1-180, O1-184 or O1-236 cDNA or O1-180, O1-184, or O1-236 antisense polynucleotides.

Since recombinant retroviruses are defective, they require assistance in order to produce infectious vector particles. This assistance can be provided, for example, by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences within the LTR. These plasmids are missing a nucleotide sequence which enables the packing mechanism to recognize an RNA transcript for encapsidation. Helper cell lines which ave deletions of the packaging signal include, but are not limited to ψ2, PA317 and PA12, for example. These cell lines produce empty virions, since no genome is packaged. If a retroviral vector is introduced into such cells in which the packaging signal is intact, but the structural genes are replaced by other genes of interest, the vector can be packaged and vector virion produced.

Alternatively NIH 3T3 or other tissue culture cells can be directly transfected with plasmids encoding the retroviral structural genes *gag*, *pol* and *env*, by conventional calcium phosphate transfection. These cells are then transfected with the vector plasmid containing the genes of interest. The resulting cells release the retroviral vector into the culture medium.

Another targeted delivery system for O1-180, O1-184 or O1-236 cDNAs or O1-180, O1-184, or O1-236 antisense polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome. Liposomes are artificial membrane vesicles which are useful as delivery vehicles *in vitro* and *in vivo*. It has been shown that large

unilamellar vesicles (LUV), which range in size from 0.2-4.0 μm can encapsulate a substantial percentage of an aqueous buffer containing large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, et al., *Trends Biochem. Sci.*, 6:77, 1981). In addition to mammalian cells, liposomes have been used for delivery of polynucleotides in plant, yeast and bacterial cells. In order for a liposome to be an efficient gene transfer vehicle, the following characteristics should be present: (1) encapsulation of the genes of interest at high exigency while not compromising their biological activity; (2) preferential and substantial binding to a target cell in comparison to non-target cells; (3) delivery of the aqueous contents of the vesicle to the target cell cytoplasm at high efficiency; and (4) accurate and effective expression of genetic information (Manning, et al., *Biotechniques*, 6:682, 1988).

The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations.

Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, sphingolipids, cerebrosides, and gangliosides. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine.

The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-specific, cell-specific, and organelle-specific. Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the

natural tendency of liposomes to distribute to cells of the reticulo-endothelial system (RES) in organs which contain sinusoidal capillaries. Active targeting, on the other hand, involves alteration of the liposome by coupling the liposome to a specific ligand such as a monoclonal antibody, sugar, glycolipid, or protein, or by changing the composition or size of the liposome in order to achieve targeting to organs and cell types other than the naturally occurring sites of localization.

The surface of the targeted delivery system may be modified in a variety of ways. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in stable association with the liposomal bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand.

Due to the expression of O1-180, O1-184 and O1-236 in the reproductive tract, there are a variety of applications using the polypeptides, polynucleotides and antibodies of the invention, related to contraception, fertility and pregnancy. O1-180, O1-184 and O1-236 could play a role in regulation of the menstrual cycle and, therefore, could be useful in various contraceptive regimens.

The following examples are intended to illustrate but not limit the invention. While they are typical of those that might be used, other procedures known to those skilled in the art may alternatively be used.

Example 1 Creation of a cDNA subtractive hybridization library

Ovaries from GDF-9-deficient mice are histologically very different from wild-type ovaries due to the early block in folliculogenesis. In particular, one layer primary follicles are relatively enriched in GDF-9-deficient ovaries and abnormal follicular nests are formed after oocyte loss. We took advantage of these differences in ovary composition and related them to alterations in gene expression patterns to clone novel ovary-expressed transcripts which are upregulated in the GDF-9-deficient ovaries.

Ovaries from either GDF-9-deficient mice (C57BL/6/129SvEv hybrid) or wild-type mice were collected and polyA+ mRNA was made from each pool. Using a modified version of the CLONTECH PCR-Select Subtraction kit, we generated a pBluescript SK+plasmid-based cDNA library which was expected to be enriched for sequences upregulated in the GDF-9-deficient ovaries. Ligations into the NotI site of pBluescript SK+ were performed with a low molar ratio of EagI-digested cDNA fragment inserts to vector to prevent multiple inserts into the vector. Transformations were performed, and > 1000 independent bacterial clones were picked and stored in glycerol at -80°C. The remainder of the ligation mix was stored at -80°C for future transformations.

Example 2 Initial sequence analysis of pOvary1 (pO1) Library inserts

We performed sequence analysis of 331 inserts from the pO1 subtractive hybridization of cDNA library. An Applied Biosystems 373 DNA Sequencer was used to sequence these clones. BLAST searches were performed using the National Center for Biotechnology Information databases. Novel sequences were analyzed for open reading frames and compared to previously identified novel sequences using DNASTAR analysis programs. A summary of the data is presented in Table 1. As shown, the majority of the clones were known genes or match mouse or human ESTs. 9.4% of the clones fail to match any known sequence in the database.

Example 3 Expression analysis and cDNA screening of ovarian-expressed genes with no known function

The functions of the pO1-library gene products which match ESTs or where there is no match are not known (Table 1). Northern blot analysis was performed on all cDNAs which failed to match sequences in any database. Additionally, sequences matching ESTs derived predominantly from mouse 2-cell embryo cDNA libraries (*e.g.*, O1-91, O1-184, and O1-236) were analyzed. The rationale for analyzing this last group of ESTs is that mRNAs expressed at high levels in oocytes may persist until the 2-cell stage and may play a role in early embryonic development including fertilization of the egg or fusion of the male and female pronuclei.

The results of the initial screen of novel ovarian genes is presented in Table 2. Northern blot analysis of 23 clones demonstrated that 8 of these clones were upregulated in the GDF-9-deficient ovary indicating the subtractive hybridization protocol used was adequate. Northern blot analysis using total RNA isolated from either adult C57BL/6/129SvEv hybrid mice (the ovarian RNA) or Swiss WEBSTER mice (all other tissues) also demonstrated that four of these clones including 2 clones which matched ESTs sequenced from 2-cell libraries were only expressed in the ovary (Figure 7). The O1-236 fragment probe (749 bp) detected a transcript of approximately 1.0 kb (Figure 7). Several clones have so far been analyzed for their ovarian localization by *in situ* hybridization analysis (Figure 8). Clones O1-180, O1-184, and O1-236 were oocyte-specific and expressed in oocytes of primary (one-layer) preantral follicles through ovulation (Figure 8).

The O1-236 gene product is oocyte-specific (Figure 9). O1-236 is not expressed in oocytes of primordial (type 2) or small type 3a follicles (Pedersen et al., *Journal of Reproduction and Fertility,* 17:555-557, 1968) (data not shown) but is first detected in oocytes of intermediate-size type 3a follicles and all type 3b follicles (*i.e.*, follicles with >20 granulosa cells surrounding the oocyte in largest cross-section). Expression of the O1-236 mRNA persisted through the antral follicle stage. Interestingly, the oocyte-specific expression pattern of the O1-236 gene product parallels the expression of other oocyte-specific genes which we have studied including *Gdf9* (McGrath et al., *Molecular Endocrinology* 9:131-136 (1995)) and bone morphogenetic protein 15 (Dube et al., *Molecular Endocrinology* 12:1809-1817, 1998).

Example 4 Cloning of ovary specific genes, including mouse *Npm2*, the mammalian ortholog of *Xenopus laevis* nucleoplasmin (*Xnpm2*).

Wild-type ovary and GDF-9-deficient ZAP Express ovary cDNA libraries were synthesized and were screened to isolate full-length cDNAs for the above-mentioned three clones. Each full-length cDNA was again subjected to database searches and analyzed for an open reading frame, initiation ATG, and protein homology. The full-length cDNAs approximate the mRNA sizes determined from Northern blot analysis.

Database searches using the predicted amino acid sequence permitted the identification of important domains (*e.g.*, signal peptide sequences, transmembrane domains, zinc fingers, etc.) which will be useful to define the possible function and cellular localization of the novel protein.

The O1-236 partial cDNA fragment identified in Example 1 was used to screen Matzuk laboratory ZAP Express (Stratagene) ovarian cDNA libraries generated from either wild-type or GDF-9 deficient ovaries as per manufacturer's instructions and as described previously (Dube, et al., *Molecular Endocrinology*, 12:1809-1817 (1998)). In brief, approximately 300,000 clones of either wild-type or GDF-9 knockout mouse ovary cDNA libraries were hybridized to [α-^{32}P] dCTP random-primed probes in Church's solution at 63°C. Filters were washed with 0.1X Church's solution and exposed overnight at -80°C.

Upon primary screening of the mouse ovarian cDNA libraries, the O1-236 cDNA fragment detected 22 positive phage clones out of 300,000 screened. Two of these clones (236-1 and 236-3), which approximated the mRNA size and which were derived from the two independent libraries, were analyzed further by restriction endonuclease digestion and DNA sequence analysis. These independent clones form a 984 bp overlapping contig (excluding the polyA sequences) and encode a 207 amino acid open reading frame (Figure 10). Including the polyA tail, this sequence approximates the 1.0 kb mRNA seen by Northern blot analysis suggesting that nearly all of the 5' UTR sequence has been isolated. When the nucleotide sequence is subjected to public database search, no significant matches were derived. However, database search with the 207 amino acid open reading frame demonstrated high homology with several nucleoplasmin homologs from several species. Interestingly, O1-236 shows highest homology with *Xenopus laevis* nucleoplasmin. At the amino acid level, O1-236 is 48% identical and 71% similar to *Xenopus laevis* nucleoplasmin (Figure 11). Based on this homology and the expression patterns of both gene products in oocytes, we have termed our gene *Npm2* since it is the mammalian

ortholog of *Xenopus laevis* nucleoplasmin [called Xnpm2 in (MacArthur et al., *Genomics* rs:137-140 (1997))]

When the Npm2 and nucleoplasmin sequences are compared, several interesting features are realized. Nucleoplasmin has a bipartite nuclear localization signal consisting of KR-$(X)_{10}$-KKKK (Dingwall, et al. *EMBO J* 6:69-74 (1987)). Deletion of either of these basic amino acid clusters in nucleoplasmin prevents translocation to the nucleus (Robbins et al. *Cell* 64:615-623) (1991)). When the Npm2 sequence is analyzed, this bipartite sequence is 100% conserved between the two proteins (Figure 11). Thus, Npm2 would be predicated to translocate to the nucleus where it would primarily function.

Also conserved between Npm2 and nucleplasmin is a long stretch of negatively charged residues. Amino acids 125-144 of Npm2 and amino acids 128-146 of nucleoplasmin are mostly glutamic acid and aspartic acid residues, with 19 out of the 20 residues for Npm2 and 16 out of the 19 residues for nucleoplasmin either Asp or Glu. This region of *Xenopus laevis* nucleoplasmin has been implicated to bind the positively charged protamines and histones. Thus, a similar function for this acidic region of Npm2 is predicted.

The last obvious feature of the Npm2 and nucleoplasmin sequences is the high number of serine and threonine residues. The Npm2 sequence contains 19 serine and 17 threonines (*i.e.*, 17.2% of the residues) and nucleoplasmin has 12 serine and 11 threonine residues (*i.e.*, 11.5% of the residues). Multiple putative phosphorylation sites are predicted from the Npm2 and nucleoplasmin sequences. Several putative phosphorylation sequences that are conserved between the two proteins are shown in Figure 11. Phosphorylation of nucleoplasmin is believed to increase its translocation to the nucleus and also its activity (Sealy et al. *Biochemistry* 25: 3064-3072 (1986); Cotten et al. *Biochemistry* 25:5063-5069 (1986); Vancurova et al. *J Cell Sci* 108:779-787 (1995); Leno et al. *J Biol Chem* 271: 7253-7256 (1996)). Similarly, phosphorylation may also alter Npm2 activity. Thus, since both *Npm2* and *Xenopus laevis* nucleoplasm are oocyte (and egg)-specific at the mRNA level and share highest identity, we conclude that Npm2 and nucleoplasmin are orthologs.

Example 5 Structure of the *Npm2* gene.

Our studies show that all three of the novel oocyte-specific cDNAs have open reading frames. As discussed above, O1-236 is the homolog of *Xenopus laevis* nucleoplasmin expressed exclusively in eggs.

One of the full length *Npm2* cDNAs (clone 236-1) was used to screen a mouse 129SvEv genomic library (Stratagene) to identify the mouse *Npm2* gene. 500,000 phage were screened and 12 positive were identified. Two of these overlapping phage clones, 236-13 and 236-14 (~37 kb of total genomic sequence), were used to determine the structure of the mouse *Npm2* gene. The mouse *Npm2* is encoded by 9 exons and spans ~6.6 kb (Figures 12 and 13). Two moderate size introns (introns 4 and 5) contribute the majority of the gene size. The initiation ATG codon resides in exon 2 and the termination codon in exon 9. The splice donor and acceptor sites (Figure 13) match well with the consensus sequences found in rodents, and all of the intron-exon boundaries conform to the "GT-AG" rule (Senapathy et al. *Methods Enzymol* 183:252-278 (1990)). A consensus polyadenylation signal sequence (AATAAA) is found upstream of the polyA tracts which are present in the two isolated cDNAs (Figure 13).

Analysis of the open reading frames of O1-180 and O1-184, fails to demonstrate any structural motifs reminiscent of known proteins, suggesting that they will be functionally unique. As with O1-236, a λFixII genomic library generated from mouse strain 129SvEv will be used for the isolation of the O1-180 and O1-184 genes. Restriction enzyme digestions, Southern blot analysis, subcloning and sequence analysis will be used to determine the genomic structure including the location and sequence of exons, exon-intron boundaries, and 5' and 3' non-translated regions. This gene structure information will be critical in generating a gene targeting vector as described below. In addition to 01-236, we have cloned 14 mouse genes from this genomic library and aided in the analysis of another 8 genes from this library. Thus, based on our previous experience, the cloning of these mouse genes will be fairly straightforward.

Example 6 Chromosomal mapping of the mouse *Npm2* gene.

Chromosomal mapping of genes in the mouse can identify candidate genes associated with spontaneous or induced mouse mutations. For example, mapping of the TGF-β family member, growth differentiation factor-5 (GDF-5), showed that it mapped to the same chromosomal location as the gene causing brachypodism in mice. Later studies showed that mutations in GDF-5 cause autosomal dominant brachydactyly type C and two types of recessive chondrodysplasia in humans. To further aid in our functional analysis of the isolated novel ovary-specific cDNAs we are mapping these mouse genes using the Research Genetics Radiation Hybrid Panel. We have mapped several other genes in our laboratory, including O1-186 (Table 3) and therefore we believe that these studies will be fairly straightforward. This information may direct us to known mutations in the mouse mapping to the same chromosomal region associated with reproductive defects. Identification of the syntenic region on the human chromosome may identify one or more of these novel ovarian genes as candidate genes for known human diseases which map to these regions.

To map the mouse *Npm2* gene, we used the Research Genetics radiation hybrid panel, The Jackson Laboratory Backcross DNA Panel Mapping Resource, and The Jackson Laboratory Mouse Radiation Hybrid Database. Forward (GCAAAGAAGC CAGTGACCAA GAAATGA) and reverse (CCTGATCATG CAAATTTTAT TGTGGCC) primers within the last exon were used to PCR amplify a 229 bp fragment from mouse but not hamster. Using these primers, the mouse *Npm2* gene was mapped to the middle of chromosome 14 (Figure 14). *Npm2* shows linkage to D14Mit32 with a LOD of 11.2 and also has a LOD of 7.8 to D14Mit203. This region is syntenic with human chromosome 8p21.

These studies will be part of our initial efforts to identify novel gene products which may be potential targets for contraceptives or treatment of infertility in human females.

As mentioned above, we have created several mouse models with defects in the ovary. We will also use ovaries from these various models (especially the GDF-9-deficient and FSH-deficient mice) to further study by *in situ* hybridization any ovary-specific genes. Thus, these additional studies may help to further define the factors which regulate their expression and the roles of these ovary-specific genes *in vivo*.

Example 7 Generation of knockout mice lacking novel ovary-expressed genes.

We will initiate studies to generate knockout mice lacking ovary-specific genes. Using the gene sequences obtained above, we will generate a targeting vector to mutate the O1-180, O1-184 and O1-236 genes in embryonic stem (ES) cells. These targeting vectors will be electroporated into the hprt-negative AB2.1 ES cell line and selected in HAT and FIAU. Clones will be processed for Southern blot analysis and screened using 5' and 3' external probes. ES cells with the correct mutation will be injected into blastocysts to generate chimeras and eventually heterozygotes and homozygotes for the mutant O1-180, O1-184 and O1-236 genes. Based on our success rate of transmission of mutant ES cell lines (28 independent mutant alleles from multiple ES cell lines) we do not anticipate any difficulties in generating heterozygotes and homozygotes for the mutant O1-180, O1-184 and O1-236 alleles.

Since expression of O1-180, O1-184 and O1-236 is limited to the ovary, we anticipate that these O1-180-deficient, O1-184-deficient and O1-236-deficient mice will be viable, but that females lacking these gene products will have fertility alterations (*i.e.*, be infertile, subfertile, or superfertile). Mutant mice will be analyzed for morphological, histological and biochemical defects similar to studies we have performed in the past. These are well within the ability of the person of ordinary skill to carry out, without undue experimentation and are expected to confirm that O1-180, O1-184 and O1-236 are key intraovarian proteins required for folliculogenesis, oogenesis, or fertilization, and that in the absence of these proteins, female mice will have increased or decreased fertility. These studies will lead us to search for human reproductive conditions with similar idiopathic phenotypes.

While this invention has been particularly shown and described with references to preferred embodiment thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described specifically therein. Such equivalents are intended to be encompassed in the scope of the claims.

Table 1. Summary of database searches of pO1 cDNA clones

pO1 cDNA Matches	Number identified	Percentage
Known Genes	180	54.4%
Mouse /Human EST	120	36.2%
RARE ESTs (1 EST match)	(8)	(2.4%)
ESTs from 2-cell library	(3)	(0.9%)
No match	31	9.4%
Total	331	100%

Table 2. **Analysis of ovarian cDNAs with no known function**

PO1 cDNA	Adult mRNA expression	Upregulated in GDF-9-deficient ovary	Database match	Further studies (in situ hybridization; chromosomal mapping)
24	Multiple	No	-	No
27	Multiple	Yes	-	Oocyte-specific by *in situ*
37	Multiple	Yes	-	No
70	Multiple	No	-	No
91			1 EST (2-cell)	
97	Multiple	No	?	No
101	Multiple	Nol	-	No
114	Multiple	No	-	No
110	Multiple	Yes	-	No
126	Multiple	Yes	-	No
180	Ovary-specific	Yes	-	Oocyte-specific by *in situ*
184	Ovary-specific	Yes	>1 EST (All 2-cell)	Oocyte-specific by*in situ*
186	Ovary-specific	Yes	-	Granulosa cell-specific by *in situ*
223	Multiple	No	-	No
224	Multiple	No	-	No

236	Ovary-specific	Yes	6 EST (2 c-cell and others)	Oocyte-specific by *in situ*
255	Multiple	No	"zinc-finger" domains	
279	Multiple	No	-	No
317	Multiple	No	-	No
330	Multiple	No	-	No
331	Multiple	No	-	No
332	Multiple	No	-	No
334	Multiple	No	-	No
371	Multiple	No	-	No

Table 3. **Analysis of partial or full-length cDNAs**

pO1 cDNA	ORF	DataBase Homolog
O1-180	361 aa	No
O1-184	426	No
O1-236	207	Yes; *Xenopus laevis nucleoplosmin homolog (81% similar)*